

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2001, 18:00:22 ; Search time 193.18 Seconds
(without alignments)
2323.997 Million cell updates/sec

Title: US-09-784-340-3_COPY_197_911

Perfect score: 715

Sequence: 1 atgaggctgacaagtcagc.....gtttatagtaagcgattag 715

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /SIDS1/gcgdata/geneseq/NA1980.DAT.*
- 2: /SIDS1/gcgdata/geneseq/NA1981.DAT.*
- 3: /SIDS1/gcgdata/geneseq/NA1982.DAT.*
- 4: /SIDS1/gcgdata/geneseq/NA1983.DAT.*
- 5: /SIDS1/gcgdata/geneseq/NA1984.DAT.*
- 6: /SIDS1/gcgdata/geneseq/NA1985.DAT.*
- 7: /SIDS1/gcgdata/geneseq/NA1986.DAT.*
- 8: /SIDS1/gcgdata/geneseq/NA1987.DAT.*
- 9: /SIDS1/gcgdata/geneseq/NA1988.DAT.*
- 10: /SIDS1/gcgdata/geneseq/NA1989.DAT.*
- 11: /SIDS1/gcgdata/geneseq/NA1990.DAT.*
- 12: /SIDS1/gcgdata/geneseq/NA1991.DAT.*
- 13: /SIDS1/gcgdata/geneseq/NA1992.DAT.*
- 14: /SIDS1/gcgdata/geneseq/NA1993.DAT.*
- 15: /SIDS1/gcgdata/geneseq/NA1994.DAT.*
- 16: /SIDS1/gcgdata/geneseq/NA1995.DAT.*
- 17: /SIDS1/gcgdata/geneseq/NA1996.DAT.*
- 18: /SIDS1/gcgdata/geneseq/NA1997.DAT.*
- 19: /SIDS1/gcgdata/geneseq/NA1998.DAT.*
- 20: /SIDS1/gcgdata/geneseq/NA1999.DAT.*
- 21: /SIDS1/gcgdata/geneseq/NA2000.DAT.*
- 22: /SIDS1/gcgdata/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	470.6	65.8	515	20 AAV87412	EST clone BR77. H
2	190.2	26.6	1976	21 AAZ95206	Human UDP-glucuron
3	190.2	26.6	2312	21 AAZ95207	Human UGT2B15 exon
4	186.8	26.1	1323	21 AAZ93193	Human UGT2B4 exon
5	186.8	26.1	2092	21 AAZ93199	Human UDP-glucuron
6	186.2	26.0	1650	21 AAC65396	Human carbohydrate
7	179	25.0	2107	19 AAV15900	Uridine diphospho-
8	172.4	24.1	1686	21 AAZ95201	Human UGT2B7 exon
9	172.4	24.1	1854	21 AAZ95200	Human UDP-glucuron
10	124	17.3	283	21 AAA87467	Rat hepatocyte car
c 11	81	11.3	936	22 AAF58252	Oligonucleotide D1

c 12	81	11.3	936	22 AAF58254	Oligonucleotide D1
c 13	81	11.3	936	22 AAF58257	Oligonucleotide D1
c 14	81	11.3	936	22 AAF58259	Oligonucleotide D2
c 15	81	11.3	936	22 AAF58262	Oligonucleotide D2
c 16	81	11.3	938	22 AAF58255	Oligonucleotide D1
17	78.6	11.0	936	22 AAF58252	Oligonucleotide D1
18	78.6	11.0	936	22 AAF58254	Oligonucleotide D1
19	78.6	11.0	936	22 AAF58257	Oligonucleotide D1
20	78.6	11.0	936	22 AAF58259	Oligonucleotide D2
21	78.6	11.0	936	22 AAF58262	Oligonucleotide D2
22	78.6	11.0	938	22 AAF58255	Oligonucleotide D1
23	69.8	9.8	264	21 AAF15707	Human prostate can
24	64.8	9.1	1048	13 AAZ33020	UGT1E Exon 1 from
25	63.2	8.8	867	21 AAZ45113	UDP-glucuronosyltr
26	55.2	7.7	867	21 AAZ45114	UDP-glucuronosyltr
27	53.6	7.5	1105	13 AAZ33022	UGT1C Exon 1 from
28	52.2	7.3	864	21 AAZ45110	UDP-glucuronosyltr
29	52.2	7.3	2351	13 AAZ27369	HUG-Brl. Homo sap
30	52	7.3	244	22 AAF58238	Oligonucleotide D1
31	52	7.3	867	21 AAZ45112	UDP-glucuronosyltr
32	49.2	6.9	861	21 AAZ45114	UDP-glucuronosyltr
33	48.8	6.8	951	21 AAZ45115	UDP-glucuronosyltr
34	48.8	6.8	1241	13 AAZ27368	UGT1F Exon 1 from
35	48.8	6.8	2368	13 AAZ27370	HUG-Brl. Homo sap
36	45.6	6.4	1120	13 AAZ33021	UGT1D Exon 1 from
c 37	43	6.0	244	22 AAF58238	Oligonucleotide D1
38	42.4	5.9	759	21 AAZ45117	UDP-glucuronosyltr
39	41.8	5.8	8318	20 AAX20264	Borrelia burgdorfe
40	40.2	5.6	5194	20 AAX25885	C.albicans alpha-I
41	40	5.6	1483	13 AAZ33023	UGT1BP Exon 1 from
c 42	38	5.3	16319	21 AAF22306	Arabidopsis thalia
43	36.8	5.1	930	21 AAZ45116	UDP-glucuronosyltr
c 44	36.2	5.1	8011	19 AAV38336	Manic-depressive i
c 45	36.2	5.1	8065	19 AAV38335	Manic-depressive i

ALIGNMENTS

RESULT 1

AAV87412
ID AAV87412 standard; cDNA; 515 BP.

XX AC AAV87412;

XX DT 27-APR-1999 (first entry)

XX DE EST clone BR77.

XX KW Expressed sequence tag; secreted protein; haematopoiesis regulator;
tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
receptor; ligand; anti-inflammatory; tumour inhibitor; ds.

XX OS Homo sapiens.

XX PN WO9845435-A2.

XX PD 15-OCT-1998.

XX PF 10-APR-1998; 98WO-US06954.

XX PR 10-APR-1997; 97US-0835913.

XX PA (GEMY) GENETICS INST INC.

XX PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;

XX PI Racie LA, Spaulding V, Treacy M;

XX XX WPI; 1999-070076/06.

XX PT New polynucleotides encoding human secreted proteins - derived from
e.g. human blood, kidney, foetal lung, placenta, testes, brain,

Query Match	26.6%	Score 190.2	DB 21	Length 1976
Best Local Similarity	56.0%	Pred. No. 5.5e-45		
Matches	407	Conservative	0	Mismatches 308; Indels 12; Gaps 2
Qy	1	atgaggctgcacaagtcagcttggatttctgtctcctgcagctctctgt---gttggc	57	
Db	8	aggatgtctcgaatggacgcgcgtctctctgtgatacagctcagttgttaactttagc	67	
Qy	58	tgtgattctctgtggaaagtcctggttggccctgtgcattgagccattggtcttaatgtc	117	
Db	68	tctggaaagctgtgaaagtgctagtgtggccacagaatacagccattggataaata	127	
Qy	118	aaggtcattctagaaagctcatagtgagagggccatgaggttaacagatttgacctca	177	
Db	128	aagcaatcctggaaagcttgttcagaggggtcatgaggtgactgtgttgacatcttcg	187	
Qy	178	aagccttggttaatgactacaggaagccttctgcattgaaatttggagtggtgcocatg	237	
Db	188	gcttctactcttgcattgcacgtataatcctgctatttaaatgagaagtttactctaca	247	
Qy	238	cc-----acaggacagacagaagaataatgaataatggttgacctagctctgaa	288	
Db	248	tctttaactaaaatgatttggagattctctcttgaaatctctcgatagatggatacat	307	
Qy	289	gctctgcagggttatcaacctggcaatcagttataaaatgattttttttgttgaa	348	
Db	308	ggtgttttcaaaaaatacatatttgggtcatttttccaaattacaagaattgtgtggaaa	367	

QY 349 ataagagaactttaaaatgatgtgtgagagctttatctacaaatcagacacattatgaag 408
D 368 tattatgactacagtaacaagcctgttaaagatgcaggtttgtaataagaacattatgatg 427
QY 409 aagctacagagaacccaactacgactgttaacgctttatagaccctgtgattccctggagac 468
D 428 aaactacaagagtcacaaagtgtgactcattctgcagatgcccttaacccctgtgtgag 487
QY 469 ctatggctgagttgtctccagctccctttgtgtcacaacttagaacttctctaagaggc 528
D 488 ctactggctgaactatttaacataccctttctgtacagttctcgtattctgtgtgctac 547
QY 529 aatatgagcgaagctgtggaaacttccagctccactttctctatgtaccctgtgctatg 588
D 548 acatttgagaagaatggtggagattctgttccctctctctatgtaccctgtgttatg 607
QY 589 acaggactaacagacagaaatgactttctggaagagtaaaaaattcaattcattcagtt 648
D 608 tcagaattaagtatcaaatgatttcatgtgagaggaataaaaaaatatgatacatatgctt 667
QY 649 ttgtccacttctggattcagagattacgactatcatttttgggaagagtttttagtaag 708
D 668 tatttgacttttggtttcaaatgtatgtatctgaagaagtggaccagtttttagtgaa 727
QY 709 gcaattag 715
D 728 gttctag 734

RESULT 3

AAZ95207
ID AAZ95207 standard; DNA; 2312 BP.
AC AAZ95207;
XX
DT 05-JUN-2000 (first entry)
DE Human UGT2B15 exon 1 nucleotide sequence.
XX
KW UDP-glucuronosyltransferase 2B15; UGT2B15; polymorphism: metabolism;
KW drug interaction; detect; human; single nucleotide polymorphism;
KW SNPs; ds.
XX
OS Homo sapiens.
XX
PN WO200006776-A1.
XX
PD 10-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US16675.
XX
PR 28-JUL-1998; 98US-0094391.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Galvin M, Miller A, Penny L, Riedy M;
XX WPI; 2000-195321/17.
XX
PT Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT genotyping individuals to predict rate of metabolism of substrates and
PT for identifying potential drug interactions
XX
PS Example 3; Page 60-61; 72pp; English.
XX
CC This sequence represents the nucleotide sequence of exon 1 of the human
CC UDP-glucuronosyltransferase 2B15 (UGT2B15) gene.
CC UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyze
CC the glucuronic acid conjugation of a wide range of endogenous and
CC exogenous substrates. The UGT2B gene subfamily encode steroid
CC metabolizing isoforms in the liver. Alteration of the expression or
CC function of UGTs may effect drug metabolism. The invention relates to

CC non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC sequence polymorphisms. Probes which detect the UGT2B locus polymorphisms
CC can be used to detect altered UGT2B metabolism of a substrate in an
CC individual. The nucleic acid molecules comprising a human UGT2B sequence
CC polymorphism can be used in screening assays for genotyping individuals,
CC also to predict their rate of metabolism of UGT2B substrate, potential
CC drug-drug interactions and adverse side effects. The polymorphisms can be
CC used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC linkage related to phenotypic variation in activity or expression of
CC UGT2B protein. The polymorphism containing nucleic acid molecules may
CC also be used for generating genetically modified non-human animals and
CC for obtaining site specific gene modification in cell lines.

XX
SQ Sequence 2312 BP; 765 A; 360 C; 414 G; 773 T; 0 other;

Query Match 26.6%; Score 190.2; DB 21; Length 2312;

Best Local Similarity 56.0%; Pred. No. 5.9e-45;

Matches 407; Conservative 0; Mismatches 308; Indels 12; Gaps 2;

QY 1 atgagctgtgacaagtcagcttctgttattctgtcctcctgcagctctctgt---gttggc 57

D 699 aggatgtctctgaaatggacgtcagctcttctgtcgtacagctcagttgttactttagc 758

QY 58 tgtgattctgtgggaagtcctgtgtgtggccctgtgacatgagccattggttaatgct 117

D 759 tctggagctgtggaaagtgctagtgtggccacagatccagccattggataatatg 818

QY 118 aaggtcattctagaagactcatgtgagggccatgagtaacagattgactcactca 177

D 819 aagacaactcctggaagactgttctcagaggggtcagtgaggtgactgtgtgacatcttcg 878

QY 178 aagcctctgttaattgactacaggaagcctctgtcattgaaatttgaggtggtccatag 237

D 879 gcttctactctgtcaatgccagtaaatcatctgtctattaaattagaagttaactaca 938

QY 238 cc-----acaggacagacagacagaagaataatgaaatat---gttgcactagctcgaat 288

D 939 tcttaactaaaaatgatttgggaagctctctctgaaaaattctcgtatagatgagatat 998

QY 289 gtcttgccaggcttatacaactggaacatcagttataaaatgaaattttttgttgaa 348

D 999 ggtgtttcaaaaaatacatttgggtcatatttttcacaaacacagaattgtgtggaa 1058

QY 349 ataagaggaactttaaaaaatgatgtgtgagagctttatctacaaatcagacacttatgaag 408

D 1059 tattatgactacagtaacaagctctgtaaaagatgcagtttgaataagaacattatgatg 1118

QY 409 aagctacagagaacccaactacagatgtaacgcttatagacccctgtgattccctggagac 468

D 1119 aaactacaagagtcacaaagtgtgactcattctgtggcagatgccttaacccctgtgtgag 1178

QY 469 ctgagctgagttgcttccagctccctttgtgtcacaacttagaacttctctaagaggc 528

D 1179 ctactggtgaaactatttaacatacccttctgtacagttctcgttctctgttggctac 1238

QY 529 aatatggcgaagctgtggaaacttccagctccactttctctatgtaccctgtgcctatg 588

D 1239 acatttgagaagaatggtgagagatttctgttccctcctctatgtaccctgtgttatg 1298

QY 589 acaggactaacagacagaatgacacttctggaagagtaaaaaatcaatgcttcaagt 648

D 1299 tcagaattaagtatcaaatgattttcattgagagagata---aaatgatgatacatgctt 1358

QY 649 ttgttccacttctgagattcagagattacagactatcattt---gaaagattttatagtaag 708

D 1359 tatttgacttttggtttcaaatattatgactgaagaact---ggaccagttttatagtaa 1418

QY 709 gcaattag 715

D 1419 gttctag 1425

[illegible]

[illegible]

Query Match		26.0%; Score 186.2; DB 21; Length 1650;
Best Local Similarity		55.4%; Pred. No. 7.2e-44;
Matches		384; Conservative 0; Mismatches 303; Indels 6; Gaps 1;
Qy	29	tctgctctgcagctctcttctgattggtgctggtattctgtggaagctctggtggtgc 88
Db	63	tctgatacagctgagctgttacttctgctggtggtggtggtggtggtggtggtggtg 122
Qy	89	cctgtgacatgagccattggtcttaattgctcaaggtcattctagaaagctctcatagtgc 148
Db	123	ccacagaattcagccactggatgaataaagacaaatcctggatgaactgtccagagag 182
Qy	149	gccatgagtaacagattgactcactcaaaagcctctggttaattgactacaggaagcctt 208
Db	183	gtcatgagtgactgtattgcatcttcagcttcattctcttcttgcacacagcccat 242
Qy	209	ctgcattgaaattgaggtgtccatagccacagggacagacagaaagaaatgaaatat 268
Db	243	ctactcttaattgaggttattctctgtatttactaaactgagttgaggtatatta 302
Qy	269	ttgttgactagctctga-----atgcttgccaggcttattcaacctggcaatcagtta 322
Db	303	tcaacagctggttaagagatggcagaaacttccaaaagacacattttggtcatatttt 362
Qy	323	taaaattaaatgattttttgttgaataagaggaacttttaaaatgatgtgtgagagct 382
Db	363	cacaagtaacaagaatcatgttgacatttaattgacatacttagaaagttctgtaaggata 422
Qy	383	ttatctacaatcagacatttatgaagagctacagaaacccaactacagatgaacgctta 442
Db	423	tagtttcaataaagaacttatgaagaactacagagagtgcaagatttgatgtgtcttg 482
Qy	443	tagacctgtgattcccggtgagacctgatgctgagttgcttccagtcctctttgtgc 502
Db	483	cagatgctgtttcccttctgtgagctgctgcccaggttacttaaaataccctttgct 542
Qy	503	tcacactagaacttctctaaagagcaatatgagcgaagctgtgggaaacttcagctc 562
Db	543	acagctccgctctctctctgctacgcgaattgaaagcagtagtgaggaacttctgttcc 602
Qy	563	cacttctctatgacctgctctgctatgacagaggaactaacagacagaatgaccttctggaaa 622
Db	603	ctcttctctatgctctgtgttatgcaagaactaagtgaccacaaatgactttcatagaga 662
Qy	623	gagtaaaaaattcagcttccagttttgttccacttctggttcaaggtattcacgactatc 682
Db	663	ggtaaaaaatgatctatgtgcttatttgaatttgggttccaaatatttgacatga 722
Qy	683	atttttgggaagagttttatagtaagcattag 715
Db	723	agaagtggaatcagttctacagtggaagttctag 755
RESULT 7		
AAV15900		
ID	AAV15900	standard; cDNA; 2107 BP.
AC	AAV15900;	
AC	AAV15900;	
DT	26-MAY-1998	(first entry)
DE	Uridine diphospho-glucuronosyltransferase 2B17 (UGT2B17) encoding cDNA.	
KW	Uridine diphospho-glucuronosyltransferase 2B17; UGT2B17; catalyze;	
KW	androstereone; androstereone-glucuronic acid; androgen; enzyme; ss.	
XX	Homo sapiens.	
XX	Location/Qualifiers	
PH	Key	1..51
FT	5'UTR	/*tag= a
FT	CDS	52..1644

FT	/*tag= b	
FT	/product= "UGTB17 enzyme"	
FT	1645..2107	
FT	/*tag= C	
XX		
PN	W09744466-A1.	
XX	27-NOV-1997.	
PF	16-MAY-1997;	97WO-CA00328.
XX		
PR	17-MAY-1996;	96US-0649319.
XX		
PA	(ENDO-) ENDORECHERCHE INC.	
XX		
PI	Beaulieu M, Belanger A, Hum DW, Levesque E.	
XX		
DR	WPI; 1998-018520/02.	
DR	P-PSDB; AAW47126.	
PT	DNA encoding uridine di-phospho-glucuronosyl-transferase 2B17 -	
PT	which catalyses conversion of androstereone to	
PT	androstereone-glucuronic acid	
XX		
PS	Claim 15; Pages 4-6; 53pp; English.	
XX		
CC	This cDNA encodes an enzyme uridine di-phosphoglucuronosyltransferase	
CC	2B17 (UGT2B17). This novel enzyme catalyses the conversion of	
CC	androstereone to androstereone-glucuronic acid. The UGT2B17 can be used to	
CC	detect anti-UGT2B17 antibodies. The antibody can be used to detect a	
CC	localised concentration of UGT2B17 or an alteration in androgen activity.	
CC	The UGT2B17 can also be used to alter the concentration of an androgenic	
CC	compound in a tissue, specifically dihydrotestosterone. An isolated	
CC	nucleotide sequence comprising at least 30 consecutive nucleotides from	
CC	the coding region of the 2107 base pair sequence, or its complement can	
CC	be used to block the synthesis of UGT2B17, e.g. an expression disrupting	
CC	sense or antisense fragment, or as a probe for a UGT2B17 coding sequence.	
XX		
SQ	Sequence 2107 BP; 657 A; 382 C; 424 G; 644 T; 0 other;	
Query Match		25.0%; Score 179; DB 19; Length 2107;
Best Local Similarity		55.0%; Pred. No. 9.5e-42;
Matches		400; Conservative 0; Mismatches 315; Indels 12; Gaps 2;
Qy	1	atgaggcttcgacagtcagcttgggtattctctgctcgcagctctctctgt---gttggc 57
Db	49	aggatgctctgaaatggatgctcagctcttctctgctgctgagtcagctcagttgttacttgc 108
Qy	58	tgtgattcttgggaaagtcctctggtggtggtggtggtggtggtggtggtggtggtggtc 117
Db	109	tctggagttgtggaaagtgctggtggtggtggtggtggtggtggtggtggtggtggtggtg 168
Qy	118	aaggtcattctagaagagctcatagtagagggccatgaggttaacagatttgacctcaatca 177
Db	169	aagacaatcctctggaaagagctgtgttcagaggggtcatgaggtgattgtgtgacattctcg 228
Qy	178	aagcctctgttaattgactacaggaagcctctcgtcattggaatttgggtggtggtcattg 237
Db	229	gcttcttcttctgccaatgcccagtaaatcatctgctatttaattagaagtttaccaca 288
Qy	238	ccacaggcagacagaaagaaatgaaatattt-----gttgacctagctgctgaat 288
Db	289	tctttaaataaaatgatttgggaagattttttatgaaaaatttcgataagatggacatat 348
Qy	289	gtcttgccaggtttatcaacctggcaatcagttataaaatgattttttttttttttttttg 348
Db	349	agtatttcaaaaaaacattttggtcatatttttcacactacacagaattgtgttgggaa 408
Qy	349	ataagaggaaacttttaaaatgatgtgtgagagcttttctacatcagacacttatgaag 408
Db	409	tattctgactataataaagctctggaagatgcagtttttgaaacaaagaacttatgaga 468

Qy	238	ccacaggacagacaagaataatgaaattattgttgacctgctgcga-----atgtc	291
Db	252	tccttaactaaactaggttgagaatttcacatgcacacattaaagagatggtcagac	311
Qy	292	ttgccaggcttatacaacctggcaatcagttataaaattaaatgatttttttttgaaata	351
Db	312	cttccaaaagatacacatttgggttatttttccacaagtagcagaatcatgtcaatattt	371
Qy	352	agaggaaactttaaaaatgatgtgtgagagccttatctcaaatcagacacattatgaagaag	411
Db	372	ggtagacataaactagaagaagttctgaaagatgagtcttccanataagaataattatgaaaaa	431
Qy	412	ctacaggaaaaccaactacgatgtacacgcttagacacctgtgatccocctggagacctg	471
Db	432	gtacaagagtcgaagatttgacgtcattttgcagatgctattttccctgtagtgcgctg	491
Qy	472	atggctgagttgttcagtcaccttttggctgcacacttagaaccttctctaaaggagccaat	531
Db	492	ctggctgagctatttaacatcacaccttggtagacagtcacactctctctcggtcacact	551
Qy	532	atggagcgaagcgttgaggaaaacttcagctccacttcccttgatcccttgatccctgtgcctatgaca	591
Db	552	tttgaagaacatagtgaggagattatttttccctccctccctcgtacctgtgttatgtca	611
Qy	592	ggactaacagacagaagaatgacctttctgaaaagagtaaaaatttcaatgcttttcacgttttg	651
Db	612	gaattaaactgatcaaatgactttcactggagaggggtaaaaaattatgatctatgtgctttac	671
Qy	652	tccactctctggatccaggattcacgactatcatttttggggagaggttttatagtaggacca	711
Db	672	tttgacttttggctcgaaaattatttgacatgaagaagtggggttcagtttttatagtgaaagt	731
Qy	712	ttag 715	
Db	732	ctag 735	
		RESULT 10	
		AAA87467	
ID		AAA87467 standard; DNA; 283 BP.	
XX		AAA87467;	
XX		08-JAN-2001 (first entry)	
XX		Rat hepatocyte carcinogenesis biomarker nucleic acid SEQ ID NO:391.	
DE		Rat; phenobarbital; carcinogenesis marker; carcinogenesis; detection;	
XX		identification; carcinogenic; probe; primer.	
KW		Rattus norvegicus.	
XX		WO200044902-A2.	
XX		03-AUG-2000.	
PD		28-JAN-2000; 2000WO-US00503.	
XX		29-JAN-1999; 99US-0118078.	
XX		(SEAR) SEARLE & CO G D.	
XX		Bunch RT, Curtis SW, Rodi CP, Morris DL;	
PI		WPI; 2000-505977/45.	
XX		New nucleic acid encoding a carcinogenic biomarker, induced by	
PT		phenobarbital treatment of rat hepatocytes, useful for identifying	
PT		carcinogenic compounds -	
XX		Claim 1; Page 184; 240pp; English.	
PS		AAA87080 to AAA87656 represent nucleic acid sequences (NL) encoding a	
CC			

05-JUN-2000 (first entry)

Human UDP-glucuronosyltransferase 2B7 nucleotide sequence.

UDP-glucuronosyltransferase 2B7; UGT2B7; polymorphism; metabolism; SNPs; drug interaction; detect; human; single nucleotide polymorphism; ds.

Homo sapiens.

W0200006776-A1.

10-FEB-2000.

22-JUL-1999; 99WO-US16675.

28-JUL-1998; 98US-0094391.

(AXYS-) AXYS PHARM INC.

Galvin M, Miller A, Penny L, Riedy M;

WPI; 2000-195321/17.

P-PSDB; AAY78934.

Novel human UDP-glucuronosyltransferase sequence, polymorphisms for genotyping individuals to predict rate of metabolism of substrates and for identifying potential drug interactions

Disclosure; Page 41-44; 72pp; English.

This sequence represents the human UDP-glucuronosyltransferase 2B7 (UGT2B7) gene. UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyse the glucuronic acid conjugation of a wide range of endogenous and exogenous substrates. The UGT2B gene subfamily encode steroid metabolizing isoforms in the liver. Alteration of the expression or function of UGTs may effect drug metabolism. The invention relates to non-chromosomal nucleic acid molecules, which comprise human UGT2B sequence polymorphisms (see AA295051-295110). Probes which detect the UGT2B locus polymorphisms can be used to detect altered UGT2B metabolism of a substrate in an individual. The nucleic acid molecules comprising a human UGT2B sequence polymorphism can be used in screening assays for genotyping individuals, also to predict their rate of metabolism of UGT2B substrate, potential drug-drug interactions and adverse side effects. The polymorphisms can be used as single nucleotide polymorphisms (SNPs) for detecting genetic linkage related to phenotypic variation in activity or expression of UGT2B protein. The polymorphism containing nucleic acid molecules may also be used for generating genetically modified non-human animals and for obtaining site specific gene modification in cell lines.

Sequence 1854 BP; 572 A; 338 C; 392 G; 552 T; 0 other;

Query Match 24.1%; Score 172.4; DB 21; Length 1854;
Best Local Similarity 54.4%; Pred. No. 7.2e-40;
Matches 394; Conservative 0; Mismatches 321; Indels 9; Gaps 2

QY 1 atgagctctgacaagtcagcttggattcttctgctcctgcagct---cttctgtgttgc 57
DB 12 aggatgctctggaatggacttcagtaatttgcatacaactgagcttctgttgc 71
QY 58 tgtggattcttctgtggaaaagtccctggtgtgcccctgtgacatgagccattggcttaatg 117
DB 72 tctgggaattctggaagggtgctgggtggtggcagcagaatacacagccattggatgaata 131
QY 118 aaggtcattctagaagctcatagtgagaggccatgaggtacaggttaactgactcactca 177
DB 132 aagacaattcctgtagtgacttattcagagagggtcatgaggtgactgtaactggtcatctca 191
QY 178 aagccttcgttaattgactacaggaagccctctctgcattgaaatttgagggtggtccatg 237
DB 192 gcttcccatctctttgtgcccacacactcatccgctctcttaaatgaaattatccca 251

PD 01-FEB-2001.
XX 26-JUL-2000; 2000WO-US20476.
XX 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX Umek RM;
XX WPI; 2001-159728/16.
DR Nucleic acids containing electron-transfer group, useful as labels in
XX hybridization assays, e.g. for genotyping, allowing repeat analyses on
XX a single surface
XX Example 6; Page 127; 159pp; English.
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
SQ

Query Match 11.3%; Score 81; DB 22; Length 936;
Best Local Similarity 1.0%; Pred. No. 1.2e-13;
Matches 6; Conservative 362; Mismatches 237; Indels 0; Gaps 0;

QY 110 ttaatgtcaagtcattcttagaagctcatgtgagagggccatgaggttaacagattga 169
DB 664 WWWWWW... 605
QY 170 ctcaactaaagccttgtaattgactacagagcctctgcattgaaattgaggtgg 229
DB 604 WWWWWW... 545
QY 230 tccatgtccacagagccttcgttaattgactacagagcctctgcattgaaattgaggtgg 229
DB 604 WWWWWW... 545
QY 230 tccatgtccacagagccttcgttaattgactacagagcctctgcattgaaattgaggtgg 229
DB 544 WWWWWW... 485
QY 290 tctgtccagccttcatacaactcgttcggaatataaattcgaattgctcctcgaatg 289
DB 184 WWWWWW... 125
QY 650 tgttccactctgattcaggattacgactatcatcttttgggaagaggttttatagtaag 709
DB 124 WWWWWW... 65

QY 710 catta 714
DB 64 WWWWW 60

RESULT 13
AAF58257/C
ID AAF58257 standard; DNA; 936 BP.
XX AAF58257;
XX 24-APR-2001 (first entry)
XX Oligonucleotide D1954.
XX Electron-transfer group; ETM; mismatch; genotyping;
KW gene expression; ss.
XX Synthetic.
OS WO200107665-A2.
PN 01-FEB-2001.
XX 26-JUL-2000; 2000WO-US20476.
XX 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX Umek RM;
XX WPI; 2001-159728/16.
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
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CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
SQ

Query Match 11.3%; Score 81; DB 22; Length 936;
Best Local Similarity 1.0%; Pred. No. 1.2e-13;
Matches 6; Conservative 362; Mismatches 237; Indels 0; Gaps 0;

QY 110 ttaatgtcaagtcattcttagaagcctcatgtgagagggccatgaggttaacagattga 169
DB 664 WWWWWW... 605
QY 170 ctcaactaaagccttcgttaattgactacagagcctctgcattgaaattgaggtgg 229
DB 604 WWWWWW... 545
QY 230 tccatgtccacagagccttcgttaattgactacagagcctctgcattgaaattgaggtgg 229
DB 544 WWWWWW... 485
QY 290 tctgtccagccttcatacaactcgttcggaatataaattcgaattgctcctcgaatg 289
DB 184 WWWWWW... 125
QY 650 tgttccactctgattcaggattacgactatcatcttttgggaagaggttttatagtaag 709
DB 124 WWWWWW... 65

Job time: 8372 sec

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PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX Umek RM;
XX WPI; 2001-159728/16.
XX Nucleic acids containing electron-transfer group, useful as labels in
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CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
SQ
Query Match 11.3%; Score 81; DB 22; Length 936;
Best Local Similarity 1.0%; Pred.No.1,2e-13;
Matches 6; Conservative 362; Mismatches 237; Indels 0; Gaps 0;
QY 110 ttaatgtcaagtcattctagaagctcatagtagagggccatgaggtaaacagtattga 169
DB 664 WWWWWW
QY 170 ctactcaaaagccttcgttaattgactacaggaagccttcgtcattgaaatttgagggtg 229
DB 604 WWWWWW
QY 230 tccatagccacagacagaaatgaatattgttgacctagctctgaaatg 289
DB 544 WWWWWW
QY 290 tctgcccagcttatacaactgagtcagttataaaattaaatgattttttgttgaaa 349
DB 484 WWWWWW
QY 350 taagaggaactttaaaatgatgtgtgagagctttatctacaactcagacacttatgaaga 409
DB 424 WWWWWW
QY 410 agctacaggaacacactacgatgtacgccttatagacctgtgacctcccgtagagacc 469
DB 364 WWWWWW
QY 470 tgatggtgagtgcttcagtcaccttttgcgtcacacttagaacctctctaaaggcca 529
DB 304 WWWWWW
QY 530 atatgagcgaagctglggaaactccagctccacttctctatgtacctgtgcctatga 589
DB 244 WWWWWW
QY 590 caggactaacagacagaatgaccttctctggaagagataaaattcaatgcttcagttt 649
DB 184 WWWWWW
QY 650 tgttccactctgattcaggattacagactatcatttttgggaagagttttatagtaagg 709
DB 124 WWWWWW
QY 710 catta 714
DB 64 WWWWWW
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